AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 7, line 9, with the following amended paragraph:

Figure 1 (A-D) shows a cDNA sequence (SEQ ID NO:1) of a hSMMyHC variant ~~using all exons (exons 1-43)~~.

Please replace the paragraph beginning on page 7, line 13, with the following amended paragraph:

Figure 3 (A-D) shows a cDNA sequence (SEQ ID NO:3) of a hSMMyHC variant ~~missing exon 42 (uses exons 1-41 and 43)~~.

Please replace the paragraph beginning on page 19, line 29, with the following amended paragraph:

The present invention provides an isolated hSMMyHC polypeptide. Preferably, the polypeptide will comprise at least 50 contiguous amino acids of SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; ~~SEQ ID NO:10, SEQ ID NO:12,~~ SEQ ID NO:10; SEQ ID NO:12; or SEQ ID NO:14. More preferably, the polypeptide comprises SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; ~~SEQ ID NO:10, SEQ ID NO:12,~~ SEQ ID NO:10; SEQ ID NO:12; or SEQ ID NO:14; or a substantially identical mutein, fragment, homolog, analog, or fusion protein thereof. According to a preferred embodiment, the polypeptide comprises the sequence -QGPSFAY- (i.e., ~~SEQ ID NO:16~~ SEQ ID NO:15; the insertion in the motor domain derived from the splice variant as described below). The polypeptides of this invention can also be fused in polypeptide linkage to a heterologous polypeptide sequence.

Please replace the paragraph beginning on page 24, line 28, with the following amended paragraph:

Bacteriophage antibody display libraries may also be screened for binding to a hSMMyHC polypeptide, such as a full-length hSMMyHC protein, a hSMMyHC fragment, or a fusion protein comprising a *hSMMyHC* polypeptide sequence comprising a hSMMyHC epitope (generally at least 5 contiguous amino acids). Generally such *hSMMyHC* peptides and the fusion protein portions consisting of hSMMyHC sequences for screening antibody libraries comprise about at least 3 to 5 contiguous amino acids of hSMMyHC, frequently at least 7 contiguous amino acids of hSMMyHC, usually comprise at least 10 contiguous amino acids of hSMMyHC, and most usually comprise a hSMMyHC sequence of at least 14 contiguous amino acids. Particularly preferred hSMMyHC epitopes are:

-QGPSFAY- (~~SEQ ID NO:16~~ SEQ ID NO:15) and -CTEQGSHP- (~~SEQ ID NO:17~~ SEQ ID NO:16).

Please amend the paragraph beginning on page 30, line 4, with the following amended paragraph:

The human SMMyHC gene has 43 exons of which are 2 exons (6 and 42) whose expression is variable and controllable by alternative splicing. Forms lacking exon 6, encoding 7 amino acids in the N-terminus, are largely found in the vasculature, forms containing exon 6 are visceral. Forms lacking exon 42 (SM1)~~,~~ are absent in fetal tissues~~;~~ forms containing exon 42 (SM2) are more constitutively expressed. The sequence of all 4 possible splice variants are found in the Drawings~~;~~

~~Fig. 1 shows the hSMMyHC isoform with all 43 exons represented (SEQ ID NO:1);~~

~~Fig. 3 shows the isoform which is missing exon 42 (SEQ ID NO:3)~~.

Please amend the paragraph beginning on page 39, line 7, with the following amended paragraph:

Provided in the invention are polynucleotides comprising a segment encoding a hSMMyHC epitope or a multiplicity of hSMMyHC epitopes. A particularly preferred polynucleotide encoding a hSMMyHC epitope of the invention ~~is~~ comprises the sequence -CAAGGCCCATCTTTTGCCTAC- ~~(SEQ ID NO:15)~~ (SEQ ID NO:17).